AMENDMENT TO THE CLAIMS

1. (Currently Amended) A process for identifying and enriching cell-specific target structures, in particular for the identification of cell-specific protein combination patterns on ~~the~~ a surface of cells and for enriching such cells, wherein said process comprises the following steps:

(a) depositing a heterogeneous cell mixture on one or plural surfaces with predefined structures, causing cells with corresponding target structures to become bound to such surface(s);

(b) removing any non-binding cells of said cell mixture from said surface(s);

(c) identifying the cell-specific target structures responsible for the binding of the cells to said surface(s);

(d) selecting and enriching cells with identical cell-specific target structures on said surface(s); and

(e) biochemically characterizing the target structures selected in procedural step (d).

2. (Original) The process as claimed in claim 1 wherein said heterogeneous cell mixture has been isolated from human or animal tissue or human or animal body fluids, or it consists of cultivated cells.

3. (Previously Presented) The process as claimed in claim 1 wherein said surface is a human or animal tissue section and/or endothelioid cells and/or protein chips and/or a cultivated piece of human or animal tissue.

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4. (Currently Amended) The process as claimed in ~~one~~ claim 1 wherein the cell-specific target structures are identified in a process comprising the following steps:

(I) automatically depositing a reagent solution Y1 that includes at least one marker molecule on said cell-specific target structure;

(II) allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

(III) removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps (I) and (II) with further reagent solutions Yn (n = 2, 3, ..., N) each containing said at least one marker molecule and/or at least another marker molecule; and

(IV) combining the marker patterns detected in step (II) to give a complex molecular combination pattern of the cell-specific target structure.

5. (Currently Amended) The process as claimed in claim 1 wherein the selected target structures are biochemically characterized in procedural step e) by means of a molecule or a molecular complex separation process~~, in particular a protein separation process~~.

6. (Currently Amended) The process as claimed in claim ~~5~~13 wherein said protein separation process is ~~a~~ 2D gel electrophoresis.

7. (Previously Presented) The process as claimed in claim 1 wherein the following procedural step is performed after procedural step d):

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d1) conducting inhibition experiments regarding one or plural ingredients of the cell-specific target structures selected in procedural step (d) for detecting a binding hierarchy of the ingredients.

8. (Original) The process as claimed in claim 7 wherein said ingredients are single or plural proteins of a cell-specific protein combination pattern.

9. (Currently Amended) The process as claimed in claim 1 wherein ~~the following procedural steps are preformed instead of~~ procedural step e) comprises the steps of:

~~(f)~~automatically depositing a reagent solution Y1 that includes at least one marker molecule on said selected and enriched cell-specific target structure;

~~(g)~~allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

~~(h)~~removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps (f) and (g) with further reagent solutions Yn (n = 2, 3, ..., N) each containing said at least one marker molecule and/or at least another marker molecule; and

~~(i)~~combining the marker patterns detected in step (g) to give a complex molecular combination pattern of the selected and enriched cell-specific target structure.

10. (Currently Amended) The process as claimed in claim 2 ~~wherein~~:

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said surface is a human or animal tissue section and/or endothelioid cells and/or protein chips and/or a cultivated piece of human or animal tissue~~;~~, and the cell-specific target structures are identified in a process comprising the following steps:

(I) automatically depositing a reagent solution Y1 that includes at least one marker molecule on said cell-specific target structure;

(II) allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

(III) removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps (I) and (II) with further reagent solutions Yn (n = 2, 3, ..., N) each containing said at least one marker molecule and/or at least another marker molecule; ~~and~~

(IV) combining the marker patterns detected in step (II) to give a complex molecular combination pattern of the cell-specific target structure;

(V) biochemically characterizing the selected target structures ~~are biochemically characterized in procedural step (e)~~ by means of ~~a molecule or molecular complex separation process, in particular a protein separation process; said protein separation process is a~~ 2D gel electrophoresis; and ~~the following procedural step is performed after procedural step (d):~~

(VI) conducting inhibition experiments regarding one or plural ingredients of the cell-specific target structures selected

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in procedural step (d) for detecting a binding hierarchy of the ingredients.

11. (Previously Presented) The process as claimed in claim 10 wherein said ingredients are single or plural proteins of a cell-specific protein combination pattern.

12. (Currently Amended) A process for identifying and enriching cell-specific target structures, in particular for the identification of cell-specific protein combination patterns on the surface of cells and for enriching such cells, wherein said process comprises the following steps:

~~(f)~~ (a) depositing a heterogeneous cell mixture on one or plural surfaces with predefined structures, causing cells with corresponding target structures to become bound to such surface(s);

~~(g)~~ (b) removing any non-binding cells of said cell mixture from said surface(s);

~~(h)~~ (c) identifying the cell-specific target structures responsible for the binding of the cells to said surface(s);

~~(i)~~ (d) selecting and enriching cells with identical cell-specific target structures on said surface(s);

~~(j)~~ (e) automatically depositing a reagent solution Y1 that includes at least one marker molecule on said selected and enriched cell-specific target structure;

~~(k)~~ (f) allowing the reagent solution Y1 to react, and automatically detecting at least one marker pattern of the target structure labeled with the reagent solution Y1;

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~~(l)~~ (g) removing said reagent solution Y1 before or after detecting the marker pattern, and repeating steps ~~(f)~~ (a) and ~~(g)~~ (b) with further reagent solutions Yn (n = 2, 3, ..., N) each containing said at least one marker molecule and/or at least another marker molecule; and

~~(m)~~ (h) combining the marker patterns detected in step ~~(g)~~ (b) to give a complex molecular combination pattern of the selected and enriched cell-specific target structure.

13. (New) The process as claimed in claim 5 wherein the molecule or molecular complex separation process is a protein separation process.

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